



1/24

SEQUENCE LISTING

<110> Abbott Laboratories
Mukerji, Pradip
Huang, Yung-Sheng
Das, Tapas
Thurmond, Jennifer M.
Pereira, Suzette L.
Leonard, Amanda E.

Sub
P1

RECEIVED
MAY 23 2002
TECH CENTER 1600/2900

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<150> US 09/769,863

<151> 2001-01-25

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<222> (6)...(6)

<223> y = t/u or c at position 6

<221> misc_feature

<222> (9)...(9)

<223> y = t/u or c at position 9

<221> misc_feature

<222> (12)...(12)

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<222> (18)...(18)

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<223> b = g or c or t/u at position 24

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<223> y = t/u or c at position 33

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<223> b = g or c or t/u at position 36

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<222> (39)...(39)
<223> h = a or c or t/u at position 39

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<223> y = t/u or c at position 6

<221> misc_feature
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<223> y = t/u or c at position 12

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<223> y = t/u or c at position 27

<221> misc_feature
<222> (33)...(33)
<223> y = tu or c at position 33

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<221> misc_feature

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<222> (41)...(41)
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<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (7)...(7)
<223> v = a or g or c at position 7

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

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<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> d = a or g or t/u at position 43

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<222> (12)...(12)
<223> r = g or a at position 12

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<222> (15)...(15)
<223> y = t/u or c at position 15

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<222> (18)...(18)
<223> r = g or a at position 18

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<222> (21)...(21)
<223> r = g or a at position 21

<221> misc_feature
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<223> s = g or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> r = g or a at position 27

<221> misc_feature
<222> (30)...(30)
<223> v = a or g or c at position 30

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<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Primer R0753

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<222> (10)...(10)
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<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature

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<222> (16)...(16)
 <223> n = a or g or c or t/u, unknown, or other at
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 <222> (18)...(19)
 <223> r = g or a at positions 18-19

<221> misc_feature
 <222> (22)...(22)
 <223> r = g or a at position 22

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24

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 <223> Primer R0754

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<221> misc_feature
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<221> misc_feature
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 <223> n = a or g or c or t/u, unknown, or other at
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 <223> n = a or g or c or t/u, unknown, or other at
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 <223> y = t/u or c at position 30

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 ctactactac tacaycayac ntayacnaay

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<220>
<223> Primer R0923

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<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer R0899

<400> 8
agcggataac aatttcacac aggaaacagc 30

<210> 9
<211> 30
<212> DNA
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<220>
<223> Primer R0939

<400> 9
cgtagtactg ctcgaggagc ttgagcgccg 30

<210> 10
<211> 31
<212> DNA
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<220>
<223> Primer R0898

<400> 10
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<210> 11
<211> 45
<212> DNA
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<220>
<223> Primer R0951

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tcaacagaat tcatggtcca ggggcaaaag gccgagaaga tctcg 45

<210> 12
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer R0960

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<212> DNA
<213> Saprolegnia diclina

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caccggggcg gcgtcgtcat gttcacgcag gccggcgaag acgcgaccga tgcgttcgct 180
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<211> 453
<212> PRT
<213> Saprolegnia diclina

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Glu His Asn Arg Gln Asp Asn Ala Trp Ile Val Ile His His Lys Val
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Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe
35 40 45
Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro
50 55 60
Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp
65 70 75 80
Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys
85 90 95
Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
100 105 110
Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys
115 120 125
Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu

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His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly		
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Leu Phe Tyr Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His His		160
	165	170
Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val		175
	180	185
Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His		190
	195	200
Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala		205
	210	215
Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser		220
225	230	235
Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe		240
	245	250
Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg		255
	260	265
Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly		270
	275	280
Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala		285
	290	295
Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala		300
305	310	315
Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala		320
	325	330
Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly		335
	340	345
Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln		350
	355	360
Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe		365
	370	375
Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val		380
385	390	395
Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys		400
	405	410
Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met		415
	420	425
Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys		430
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Glu Phe Pro Ala Met		445
450		

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<220>
 <223> Primer RO851

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<210> 16
 <211> 28
 <212> DNA

9/24

<213> Artificial Sequence

<220>

<223> Primer R0941

<400> 16

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<210> 17

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Primer R0953

<400> 17

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<210> 18

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Primer R0956

<400> 18

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<210> 19

<211> 1413

<212> DNA

<213> Saprolegnia diclina

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28

42

46

10/24

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<213> Saprolegnia diclina

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20 25 30
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35 40 45
Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val
50 55 60
Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His
65 70 75 80
Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly
85 90 95
Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly
100 105 110
Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn
115 120 125
Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val
130 135 140
Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr
145 150 155 160
Ile Phe Ala Leu Gln Leu Ala Ala Ala Ala Leu Phe Gly Val Cys Gln
165 170 175
Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr
180 185 190
Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp
195 200 205
Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val
210 215 220
Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro
225 230 235 240
Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe
245 250 255
Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly
260 265 270
Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly
275 280 285
Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr
290 295 300
Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val
305 310 315 320
Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala
325 330 335
Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn
340 345 350
Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp
355 360 365
Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys

370						375						380					
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465					470												

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 <213> Homo sapiens

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<210> 22
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 <212> DNA
 <213> Mortierella alpina

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<213> Artificial Sequence

<220>

<223> Primer R0936

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<213> Artificial Sequence

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42

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<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Primer R0949

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39

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<211> 41

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<213> Artificial Sequence

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<223> Primer R0950

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41

<210> 28

<211> 1320

<212> DNA

<213> *Thraustochytrium aureum*

<400> 28

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atgggacgcg gcggcgaagg tcaggtgaac agcgcgcagg tggcacaagg cgggtgcggga 60
acgcgaaaga cgatcctgat cgagggcgag gtctacgatg tcaccaactt taggcacccc 120
ggcgggtcga tcatcaagtt tctcacgacc gacggcaccg aggtgtgtga cgcgacgaac 180
gcgtttcgcg agtttcaactg ccggtcgggc aaggcggaaa agtacctcaa gagcctgccc 240
aagctcggcg cgccgagcaa gatgaagttt gacgccaagg agcaggcccg gcgcgacgcg 300
atcacgcgag actacgtcaa gctgcgcgag gagatggtgg ccgagggcct cttcaagccc 360
gcgcccctcc acattgtcta caggtttgcg gagatcgag ccctgttcgc ggccctcgttc 420
tacctgtttt cgatgcgcgg aaacgtgttc gccacgctcg cggccatcgc agtcggggggc 480
atcgcgagg ggcgtgcgg ctgggtcatg caccagtgcg gacacttctc gatgaccggg 540
tacatccgcg ttgacgtgag cctgcaggag ctgggtgtac gcgtgggggtg ctcgatgtcg 600
gcgagctggt ggcgcgttca gcacaacaag caccacgcga ccccgagaa actcaagcac 660
gacgtcgacc tcgacaccct gccgctcggt gcgttcaacg agaagatcgc cgccaagggtg 720
cgccccggct cgttccaggc caagtggctc tcggcgcagg cgtacatttt tgcgcgggtg 780
tctgtcttcc tggttggtct cttctggacc ctgtttctgc acccgcgcca catgccgcgc 840
acgagccact ttgctgagat ggccgcgcgc gcggtgcgcg tcgtggggtg ggcggcgctc 900
atgcactcgt tcgggtacag cgggagcgac tcgttcggtc tctacatggc cacctttggc 960
tttggttgca cctacatctt caccaacttt gcggtcagcc acacgcacct cgacgtcacc 1020
gagccggacg agttcctgca ctgggtcgag tacgcgcgcg tgcacacgac caacgtgtcc 1080
aacgactcgt ggttcatcac ctgggtgatg tcgtacctca actttcagat cgagcaccac 1140
ctctttccgt cgctgcccc gctcaacgcc ccgcgcgtcg ccccgcgcgt ccgcgccttc 1200
ttcgagaagc acggcatggc ttacgacgag cgcccgatcc ttaccgcgct tggcgacacg 1260
tttgccaacc tgcacgccgt gggccaaaac gcgggcccagg cggcggccaa ggccgcttag 1320

```

<210> 29

<211> 439

<212> PRT

<213> *Thraustochytrium aureum*

<400> 29

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Met Gly Arg Gly Gly Glu Gly Gln Val Asn Ser Ala Gln Val Ala Gln
 1          5          10          15
Gly Gly Ala Gly Thr Arg Lys Thr Ile Leu Ile Glu Gly Glu Val Tyr
 20          25          30
Asp Val Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Phe Leu
 35          40          45
Thr Thr Asp Gly Thr Glu Ala Val Asp Ala Thr Asn Ala Phe Arg Glu
 50          55          60
Phe His Cys Arg Ser Gly Lys Ala Glu Lys Tyr Leu Lys Ser Leu Pro
 65          70          75          80
Lys Leu Gly Ala Pro Ser Lys Met Lys Phe Asp Ala Lys Glu Gln Ala
 85          90          95
Arg Arg Asp Ala Ile Thr Arg Asp Tyr Val Lys Leu Arg Glu Glu Met
100          105          110
Val Ala Glu Gly Leu Phe Lys Pro Ala Pro Leu His Ile Val Tyr Arg
115          120          125
Phe Ala Glu Ile Ala Ala Leu Phe Ala Ala Ser Phe Tyr Leu Phe Ser
130          135          140
Met Arg Gly Asn Val Phe Ala Thr Leu Ala Ala Ile Ala Val Gly Gly

```

[illegible]

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<210> 30
<211> 1338
<212> DNA
<213> Thraustochytrium aureum
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<400> 30						
gaattcacca	tgggtcgcg	agcacagga	gagccaagc	aggccacaga	gctgaagagc	60
agcccaagt	agcagcgtaa	ggtgttgctc	attgacgggc	agctgtacga	tgcaaccaac	120
ttcaggcatc	ctggtggctc	catcatcaaa	tatttgtgca	ccgatggcaa	ggaggtagtt	180
gatgcaaccg	aagcgtacaa	ggagttcca	tgcagatcct	cgaaggcggt	caagtacctc	240
aactccctgc	caaagatcga	cggcccaatc	aagtacaaat	acgacgcaa	ggagcaggct	300
cgccatgaca	aactcacgag	ggagtatgta	gctctccgcy	aacagctcgt	caaggaggga	360
tactttgacc	ccagcccgct	ccacattatc	tacagatgcy	ccgagttggc	agccatgttc	420
gctctctcgt	tctacctttt	ctccttcaag	ggtaacgtca	tggccactat	tgctgccatc	480
gtgattgggg	ggtgcgtgca	gggtcgttgt	gggtggctca	tgcattgaag	tggccattac	540
agcatgaccg	gaaacatccc	tgttgacttg	cgcttccaag	agtttttgta	cggaacttgg	600
tgtggcatga	gcggggcctt	gtggagaagc	cagcacaca	agcaccacgc	caccccccaa	660
aagctcaagc	atgacgttga	tttggaact	cttctcttgc	tcgcctggaa	cgagaaaatt	720

```

gccgctcgcg tcaagccagg tagcttccag gcaaagtggc ttcattctcca gggatacatc 780
tttgccccag tctcctgcct tctcgttggg ctcttctgga ctttgtactt gcatacctcgc 840
cacatgatcc gcaccaagcg caacttcgag atattttctg tgcgtctgcg ctacgtatgc 900
tggttctcgc ttcttttgag catggggtac actgtcggag agtctctggg tctctatgtg 960
cttacttttg gacttggctg tacctacatc tttacgcatt ttgctgtaag ccacaccac 1020
ttgccagtgt ccgaggagga cgagtacctg cactgggtcg agtacgctgc gctgcacacc 1080
acgaacgttg ccatcgactc gtacgttgtc acctggctga tgagctacct caactttcag 1140
atcgagcacc acttggtccc ttgctgcccg cagttccgcc accctgcaat ctcttctcgc 1200
gtcaagaaac ttttcgagga caatggtctg gtatacgacg cccgctcata cgtccaggcg 1260
ctcaaggata ccttcggcaa cctacacgaa gtgggcgtca acgctggcca agctgccaaag 1320
agcgagtaag atctcgag 1338

```

<210> 31

<211> 439

<212> PRT

<213> *Thraustochytrium aureum*

<400> 31

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Met Gly Arg Gly Ala Gln Gly Glu Pro Arg Gln Ala Thr Glu Leu Lys
1      5      10      15
Ser Ser Pro Ser Glu Gln Arg Lys Val Leu Leu Ile Asp Gly Gln Leu
20      25      30
Tyr Asp Ala Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Tyr
35      40      45
Leu Cys Thr Asp Gly Lys Glu Val Val Asp Ala Thr Glu Ala Tyr Lys
50      55      60
Glu Phe His Cys Arg Ser Ser Lys Ala Val Lys Tyr Leu Asn Ser Leu
65      70      75      80
Pro Lys Ile Asp Gly Pro Ile Lys Tyr Lys Tyr Asp Ala Lys Glu Gln
85      90      95
Ala Arg His Asp Lys Leu Thr Arg Glu Tyr Val Ala Leu Arg Glu Gln
100     105     110
Leu Val Lys Glu Gly Tyr Phe Asp Pro Ser Pro Leu His Ile Ile Tyr
115     120     125
Arg Cys Ala Glu Leu Ala Ala Met Phe Ala Leu Ser Phe Tyr Leu Phe
130     135     140
Ser Phe Lys Gly Asn Val Met Ala Thr Ile Ala Ala Ile Val Ile Gly
145     150     155     160
Gly Cys Val Gln Gly Arg Cys Gly Trp Leu Met His Glu Ala Gly His
165     170     175
Tyr Ser Met Thr Gly Asn Ile Pro Val Asp Leu Arg Leu Gln Glu Phe
180     185     190
Leu Tyr Gly Ile Gly Cys Gly Met Ser Gly Ala Trp Trp Arg Ser Gln
195     200     205
His Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp
210     215     220
Leu Asp Thr Leu Pro Leu Val Ala Trp Asn Glu Lys Ile Ala Arg Arg
225     230     235     240
Val Lys Pro Gly Ser Phe Gln Ala Lys Trp Leu His Leu Gln Gly Tyr
245     250     255
Ile Phe Ala Pro Val Ser Cys Leu Leu Val Gly Leu Phe Trp Thr Leu
260     265     270
Tyr Leu His Pro Arg His Met Ile Arg Thr Lys Arg Asn Phe Glu Ile
275     280     285
Phe Ser Val Ala Leu Arg Tyr Val Cys Trp Phe Ser Leu Leu Leu Ser
290     295     300
Met Gly Tyr Thr Val Gly Glu Ser Leu Gly Leu Tyr Val Leu Thr Phe

```

[illegible]

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<210> 32
<211> 1381
<212> DNA
<213> Thraustochytrium aureum
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[illegible]

```
<210> 33
<211> 456
<212> PRT
<213> Thraustochytrium aureum
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<400> 33
Met Gly Arg Gly Gly Glu Lys Ser Glu Val Asp Gln Val Gln Pro Gln
1 5 10 15

Lys Thr Glu Gln Leu Gln Lys Ala Lys Trp Glu Asp Val Val Arg Ile
 20 25 30
 Asn Gly Val Glu Tyr Asp Val Thr Asp Tyr Leu Arg Lys His Pro Gly
 35 40 45
 Gly Ser Val Ile Lys Tyr Gly Leu Ala Asn Thr Gly Ala Asp Ala Thr
 50 55 60
 Ser Leu Phe Glu Ala Phe His Met Arg Ser Lys Lys Ala Gln Met Val
 65 70 75 80
 Leu Lys Ser Leu Pro Lys Arg Ala Pro Val Leu Glu Ile Gln Pro Asn
 85 90 95
 Gln Leu Pro Glu Glu Gln Thr Lys Glu Ala Glu Met Leu Arg Asp Phe
 100 105 110
 Lys Lys Phe Glu Asp Glu Ile Arg Arg Asp Gly Leu Met Glu Pro Ser
 115 120 125
 Phe Trp His Arg Ala Tyr Arg Leu Ser Glu Leu Val Gly Met Phe Thr
 130 135 140
 Leu Gly Leu Tyr Leu Phe Ser Leu Asn Thr Pro Leu Ser Ile Ala Ala
 145 150 155 160
 Gly Val Leu Val His Gly Leu Phe Gly Ala Phe Cys Gly Trp Cys Gln
 165 170 175
 His Glu Ala Gly His Gly Ser Phe Phe Tyr Ser Leu Trp Trp Gly Lys
 180 185 190
 Arg Val Gln Ala Met Leu Ile Gly Phe Gly Leu Gly Thr Ser Gly Asp
 195 200 205
 Met Trp Asn Met Met His Asn Lys His His Ala Ala Thr Gln Lys Val
 210 215 220
 His His Asp Leu Asp Ile Asp Thr Thr Pro Phe Val Ala Phe Phe Asn
 225 230 235 240
 Thr Ala Phe Glu Lys Asn Arg Trp Lys Gly Phe Ser Lys Ala Trp Val
 245 250 255
 Arg Phe Gln Ala Phe Thr Phe Ile Pro Val Thr Ser Gly Met Ile Val
 260 265 270
 Met Leu Phe Trp Leu Phe Phe Leu His Pro Arg Arg Val Val Gln Lys
 275 280 285
 Lys Asn Phe Glu Glu Gly Phe Trp Met Leu Ser Ser His Ile Val Arg
 290 295 300
 Thr Tyr Leu Phe His Leu Val Thr Gly Trp Glu Ser Leu Ala Ala Cys
 305 310 315 320
 Tyr Leu Val Gly Tyr Trp Ala Cys Met Trp Val Ser Gly Met Tyr Leu
 325 330 335
 Phe Gly His Phe Ser Leu Ser His Thr His Met Asp Ile Val Glu Ala
 340 345 350
 Asp Val His Lys Asn Trp Val Arg Tyr Ala Val Asp His Thr Val Asp
 355 360 365
 Ile Ser Pro Ser Asn Pro Leu Val Cys Trp Val Met Gly Tyr Leu Asn
 370 375 380
 Met Gln Thr Ile His His Leu Trp Pro Ala Met Pro Gln Tyr His Gln
 385 390 395 400
 Val Glu Val Ser Arg Arg Phe Ala Ile Phe Ala Lys Lys His Gly Leu
 405 410 415
 Asn Tyr Arg Val Val Ser Tyr Phe Glu Ala Trp Arg Leu Met Leu Gln
 420 425 430
 Asn Leu Ala Asp Val Gly Ser His Tyr His Glu Asn Gly Val Lys Arg
 435 440 445
 Ala Pro Lys Lys Ala Lys Ala Gln
 450 455

<210> 34
 <211> 1329
 <212> DNA
 <213> Isochrysis galbana

<400> 34
 atggtggcag gcaaatacagg cgctgcccgc cacgtgactc acagctcgac attgccccgt 60
 gagtaccatg gcgcgaccaa cgactcgcgc tctgaggcgg ccgacgtcac cgtctctagc 120
 atcgatgctg aaaaggagat gatcatcaac ggccgcgtgt atgacgtgtc gtcattttgtg 180
 aagcggcacc caggtggctc ggtgatcaag ttccagctgg gcgcgacgc gagcgacgcg 240
 tacaacaact ttacgtccg ctccaagaag gcggacaaga tgctgtattc gctcccgtcc 300
 cggccggccg aggcgggcta cgcccaggac gacatctccc gcgactttga gaagctgcgc 360
 ctcgagctga aggaggaggg ctacttcgag cccaacctgg tgcacgtgag ctacaggtgt 420
 gtggagggttc ttgccatgta ctgggctggc gtccagctca tctgggtccg gtactgggtc 480
 ctcggcgcga tcgtggccgg cattgcgcag ggccgctcgc gctgggtcca gcatgagggg 540
 gggcactact cgctcaccgg caacatcaag atcgaccggc atctgcagat ggccatctat 600
 gggcttggct gcggcatgtc gggctgctac tggcgcaacc agcacaacaa gcaccacgcc 660
 acgcgcgaga agctcgggac cgaccccgac ctgcagacga tgccgctggg ggccctccac 720
 aagatcgctc gcgccaaggc gcgaggcaag ggcaaggcgt ggctggcgtg gaagcgccg 780
 ctcttctttg gcgggatcat ctgctcgtc gtctctttcg gctggcagtt cgtgctccac 840
 cccaaccacg cgctgcgcgt gcacaatcac ctggagctcg cgtacatggg cctgcggtac 900
 gtgctgtggc acctggcctt tggccacctc gggctgctga gctcgctccg cctgtacgcc 960
 ttttaactgg ccgtggcggc caactacatc ttcaccaact tcgcgctctc gcacacccac 1020
 aaggacgtcg tcccgcccac caagcacatc tcgtgggcac tctactcggc caaccacacg 1080
 accaactgct ccgactcggc ctttgtcaac tgggtgatgg cctacctcaa cttccagatc 1140
 gagcaccacc tcttcccgtc gatgccgcag tacaaccacc ccaagatcgc ccgcgggtg 1200
 cgccgcgtct tcgagaagca cggggctcag tatgacgtcc ggccatacct ggagtgttt 1260
 cgggtcacgt acgtcaacct gctcgccgta ggcaaccggc agcactccta ccacgagcac 1320
 acgcactag 1329

<210> 35
 <211> 442
 <212> PRT
 <213> Isochrysis galbana

<400> 35
 Met Val Ala Gly Lys Ser Gly Ala Ala His Val Thr His Ser Ser
 1 5 10 15
 Thr Leu Pro Arg Glu Tyr His Gly Ala Thr Asn Asp Ser Arg Ser Glu
 20 25 30
 Ala Ala Asp Val Thr Val Ser Ser Ile Asp Ala Glu Lys Glu Met Ile
 35 40 45
 Ile Asn Gly Arg Val Tyr Asp Val Ser Ser Phe Val Lys Arg His Pro
 50 55 60
 Gly Gly Ser Val Ile Lys Phe Gln Leu Gly Ala Asp Ala Ser Asp Ala
 65 70 75 80
 Tyr Asn Asn Phe His Val Arg Ser Lys Lys Ala Asp Lys Met Leu Tyr
 85 90 95
 Ser Leu Pro Ser Arg Pro Ala Glu Ala Gly Tyr Ala Gln Asp Asp Ile
 100 105 110
 Ser Arg Asp Phe Glu Lys Leu Arg Leu Glu Leu Lys Glu Glu Gly Tyr
 115 120 125
 Phe Glu Pro Asn Leu Val His Val Ser Tyr Arg Cys Val Glu Val Leu
 130 135 140
 Ala Met Tyr Trp Ala Gly Val Gln Leu Ile Trp Ser Gly Tyr Trp Phe
 145 150 155 160
 Leu Gly Ala Ile Val Ala Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu

165 170 175
 Gln His Glu Gly Gly His Tyr Ser Leu Thr Gly Asn Ile Lys Ile Asp
 180 185 190
 Arg His Leu Gln Met Ala Ile Tyr Gly Leu Gly Cys Gly Met Ser Gly
 195 200 205
 Cys Tyr Trp Arg Asn Gln His Asn Lys His His Ala Thr Pro Gln Lys
 210 215 220
 Leu Gly Thr Asp Pro Asp Leu Gln Thr Met Pro Leu Val Ala Phe His
 225 230 235 240
 Lys Ile Val Gly Ala Lys Ala Arg Gly Lys Gly Lys Ala Trp Leu Ala
 245 250 255
 Trp Gln Ala Pro Leu Phe Phe Gly Gly Ile Ile Cys Ser Leu Val Ser
 260 265 270
 Phe Gly Trp Gln Phe Val Leu His Pro Asn His Ala Leu Arg Val His
 275 280 285
 Asn His Leu Glu Leu Ala Tyr Met Gly Leu Arg Tyr Val Leu Trp His
 290 295 300
 Leu Ala Phe Gly His Leu Gly Leu Leu Ser Ser Leu Arg Leu Tyr Ala
 305 310 315 320
 Phe Tyr Val Ala Val Gly Gly Thr Tyr Ile Phe Thr Asn Phe Ala Val
 325 330 335
 Ser His Thr His Lys Asp Val Val Pro Thr Lys His Ile Ser Trp
 340 345 350
 Ala Leu Tyr Ser Ala Asn His Thr Thr Asn Cys Ser Asp Ser Pro Phe
 355 360 365
 Val Asn Trp Trp Met Ala Tyr Leu Asn Phe Gln Ile Glu His His Leu
 370 375 380
 Phe Pro Ser Met Pro Gln Tyr Asn His Pro Lys Ile Ala Pro Arg Val
 385 390 395 400
 Arg Ala Leu Phe Glu Lys His Gly Val Glu Tyr Asp Val Arg Pro Tyr
 405 410 415
 Leu Glu Cys Phe Arg Val Thr Tyr Val Asn Leu Leu Ala Val Gly Asn
 420 425 430
 Pro Glu His Ser Tyr His Glu His Thr His
 435 440

<210> 36

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0838

<221> misc_feature

<222> (7)...(7)

<223> v = a or g or c at position 7

<221> misc_feature

<222> (10)...(10)

<223> r = g or a at position 10

<221> misc_feature

<222> (13)...(13)

<223> s = g or c at position 13

<221> misc_feature

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<222> (16)...(16)
<223> r = g or a at position 16

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (22)...(22)
<223> y = t/u or c at position 22

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
<223> r = g or a at position 31

<400> 36
catggtvggr aasagrtgrt gytcratctg rtagtt
36

<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1065

<400> 37
cgacaagagg aagagtgtcc aaatc
25

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1064

<400> 38
cgccttcaag agtttttgta cggaattggg
30

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1097

<400> 39
cttgtaccat gggtcgcgga gcacagggag
30

<210> 40
<211> 30

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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer RO1098

 <400> 40
 tgaagcttac tcgctcttgg cagcttggcc 30

 <210> 41
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer RO1107

 <400> 41
 ttttaaccatg ggccgcggcg gcgagaaaag 30

 <210> 42
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer RO1108

 <400> 42
 gggaagaagc tttctactgc gccttggctt tctttg 36

 <210> 43
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer RO1235

 <400> 43
 cgaagtgggt gaagatgtag gtgccg 26

 <210> 44
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer RO1232

 <400> 44
 gagcgacgcg tacaacaact ttcacgt 27

 <210> 45
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 45
 cgactggagc acgaggacac tga 23

 <210> 46
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> GeneRacer 3 Prime Primer

 <400> 46
 gctgtcaacg atacgctacg taacg 25

 <210> 47
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nested Primer RO1234

 <400> 47
 agctccaggt gattgtgcac gcgcag 26

 <210> 48
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer RO1233

 <400> 48
 gactttgaga agctgcgcct cgagctg 27

 <210> 49
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nested 5 Prime Primer

 <400> 49
 ggacactgac atggactgaa ggagta 26

 <210> 50
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Nested 3 Prime Primer
 <400> 50
 cgctacgtaa cggcatgaca gtg 23
 <210> 51
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer R01309
 <400> 51
 atgatggaat tcatggtggc aggcaaatca ggcgc 35
 <210> 52
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer R01310
 <400> 52
 aataatgtcg acctagtgcg tgtgctcgtg gtagg 35
 <210> 53
 <211> 14
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Consensus Peptide Sequence
 <400> 53
 Val Tyr Asp Val Thr Glu Trp Val Lys Arg His Pro Gly Gly
 1 5 10
 <210> 54
 <211> 15
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Consensus Peptide Sequence
 <400> 54
 Gly Ala Ser Ala Asn Trp Trp Lys His Gln His Asn Val His His
 1 5 10 15
 <210> 55
 <211> 12
 <212> PRT
 <213> Artificial Sequence
 <220>

24/24

<223> Consensus Peptide Sequence

<400> 55

Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met
1				5					10		